

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**



## SEQUENCE LISTING

<10> MOECKEL, Bettina  
BATHE, Brigitte  
HERMANN, Thomas  
PFEFFERLE, Walter  
BINDER, Michael

<120> Nucleotide sequences coding for the rpoB gene

<130> 219774US0XCIP

<140> new application  
<141> 2002-02-19

<150> DE 10107229.5  
<151> 2001-02-16

<150> US 09/887052  
<151> 2001-06-25

<160> 12

<170> PatentIn version 3.1

<210> 1  
<211> 5099  
<212> DNA  
<213> Corynebacterium glutamicum

<220>  
<221> CDS  
<222> (702)..(4196)  
<223>

<400> 1  
acaatgtgac tcgtgatttt tgggtggatc agcgtaccgg tttggttgtc gatctagctg 60  
aaaatattga tgatTTTAC ggcgaccgca gcggccagaa gtacgaacag aaattgcttt 120  
tcgacgcctc cctcgacgat gcagctgtct ctaagctggc tgcacaggcc gaaagcatcc 180  
ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggt gcggtattgg 240  
ctctcggtgg cctggccggg tgggggggg cggtggaa gaaacgtcga gaagcttaac 300  
ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tgTTTGTAG 360  
ggTgcctcgT agaaggggTC aagaagattt ctggaaacg cggccgtgcg gttggTTGCT 420  
aatagcacgc ggagcaccag atgaaaaatc tccccTTAC ttTcgcgCgC gattggata 480  
ctctgagtcg ttgcgttgga attcgtgact ctTTTGTGTT CCTGTAGCgC caagaccttG 540  
atcaaggtgg tttaaaaaaa ccgatttgac aaggtcattc agtgcTatct ggagtgcTTc 600

agggggatcg ggccctcag cagaccaatt gctaaaaat accagcgtt ttgatctgca	660
cttaatggcc ttgaccagcc aggtgcaatt acccggtga g gtg ctg gaa gga ccc Val Leu Glu Gly Pro	716
1 5	
atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly	764
10 15 20	
gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val	812
25 30 35	
ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly	860
40 45 50	
acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala	908
55 60 65	
cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Leu Ser Pro Ile	956
70 75 80 85	
cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe	1004
90 95 100	
gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn	1052
105 110 115	
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr	1100
120 125 130	
ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met	1148
135 140 145	
acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val	1196
150 155 160 165	
agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp	1244
170 175 180	
aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg	1292
185 190 195	
ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val	1340
200 205 210	

cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct		1388	
Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala			
215	220	225	
ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa		1436	
Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu			
230	235	240	245
atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag		1484	
Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu			
250	255	260	
gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc		1532	
Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr			
265	270	275	
cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag		1580	
Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys			
280	285	290	
cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc		1628	
Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu			
295	300	305	
ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac		1676	
Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp			
310	315	320	325
atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc		1724	
Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg			
330	335	340	
gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac		1772	
Val Met Thr Ser Pro Asn Gly Glu Ile Pro Val Glu Thr Asp Asp			
345	350	355	
atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc		1820	
Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile			
360	365	370	
cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt		1868	
Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg			
375	380	385	
gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg		1916	
Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu			
390	395	400	405
atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act		1964	
Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr			
410	415	420	
tcc cag ctg tct cag ttc atg gac cag aac aac tcc ctg tct ggt ttg		2012	
Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn Ser Leu Ser Gly Leu			
425	430	435	

act cac aag cgt cgt tcg gct ctg ggc ccg ggt ggt ctg tcc cgt	2060
Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg	
440 445 450	
gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc	2108
Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly	
455 460 465	
cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156
Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile	
470 475 480 485	
ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204
Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu	
490 495 500	
acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252
Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp	
505 510 515	
tac ctt acc gct gat gag gaa gac cgc ttc gtt gtt gcg cag gca aac	2300
Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn	
520 525 530	
acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348
Thr His Tyr Asp Glu Glu Asn Ile Thr Asp Glu Thr Val Thr Val	
535 540 545	
cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396
Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp	
550 555 560 565	
tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444
Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met	
570 575 580	
att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492
Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala	
585 590 595	
aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540
Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe	
600 605 610	
gtg ggc acc ggt atg gag cag cgc gca tac gac gcc ggc gac ctg	2588
Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu	
615 620 625	
gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636
Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe	
630 635 640 645	
atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684
Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg	
650 655 660	
aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg	2732

Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu			
665	670	675	
gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt		2780	
Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly			
680	685	690	
cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt		2828	
Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val			
695	700	705	
gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc		2876	
Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu			
710	715	720	725
aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag		2924	
Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu			
730	735	740	
gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc		2972	
Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile			
745	750	755	
acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac		3020	
Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp			
760	765	770	
gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc		3068	
Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile			
775	780	785	
ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccc gaa		3116	
Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu			
790	795	800	805
gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc		3164	
Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg			
810	815	820	
gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc		3212	
Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly			
825	830	835	
gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc		3260	
Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val			
840	845	850	
aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac		3308	
Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp			
855	860	865	
ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa		3356	
Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys			
870	875	880	885
att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt		3404	
Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val			

890	895	900	
gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly 905 910 915			3452
cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser 920 925 930			3500
gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro 935 940 945			3548
gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val 950 955 960 965			3596
ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser 970 975 980			3644
cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala 985 990 995			3692
acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val 1000 1005 1010			3737
tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp 1015 1020 1025			3782
gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr 1030 1035 1040			3827
cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe 1045 1050 1055			3872
ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr 1060 1065 1070			3917
aca ctt cag gag ctg ctg acc atc aag tct gat gac gtc gtt ggc Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly 1075 1080 1085			3962
cgt gtc aag gtc tac gaa gca att gtc aag ggc gag aac atc ccg Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro 1090 1095 1100			4007
gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu 1105 1110 1115			4052

cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act	4097
Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr	
1120 1125 1130	
cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142
Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly	
1135 1140 1145	
gcc tca ctt ggc atc aac ctg tcc cgt gac gag cgt tcc gac gcc	4187
Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu Arg Ser Asp Ala	
1150 1155 1160	
gac acc gca tagcagatca gaaaacaacc gctagaaaatc aagccataca	4236
Asp Thr Ala	
1165	
tcccccggac attgaagaga ttttctgggg ggaaagggag ttttacgtgc tcgacgtaaa	4296
cgtcttcgat gagctccgca tcggcctggc caccggcgcac gacatccgccc gttggtccaa	4356
gggtgaggc aagaagccgg agaccatcaa ctaccgaacc ctcaagcctg agaaggacgg	4416
tctgttctgc gagcgtatct tcggtccaac tcgctactgg gagtgcgcct gcggtaagta	4476
caagcgtgtc cgctacaagg gcatcatctg tgaacgctgt ggcgttgagg tcaccaagtc	4536
caaggtgcgc cgtgagcgca tgggacacat tgagctcgct gcaccagtaa cccacatttgc	4596
gtacttcaag ggcgttccat cacgcctcggtt gaccttgctc caaaggacct	4656
ggacctcatc atctacttcg gtgcgaacat catcaccaggc gtggacgaag aggctcgcca	4716
cagcgaccag accactcttg aggcagaaat gcttctggag aagaaggacg ttgaggcaga	4776
cgcagagtct gacattgctg agcgtgctga aaagctcgaa gaggatcttgc tgcacttgc	4836
ggcagctggc gctaaggccg acgctcgccg caaggttcag gctgctgccc ataaggaaat	4896
gcagcacatc cgtgagcggtg cacagcgca aatcgatcg ttcgatgagg tctggcagac	4956
cttcatcaag cttgctccaa agcagatgat ccgcgttgag aagctctacg atgaactgat	5016
cgaccgctac gaggattact tcaccgggtgg tatgggtgca gagtccatttgc aggctttgat	5076
ccagaacttc gaccttgatg ctg	5099

<210> 2  
 <211> 1165  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 2

Val Leu Glu Gly Pro Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val  
 1 5 10 15

Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser  
20 25 30

Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr  
35 40 45

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu  
50 55 60

Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu  
65 70 75 80

Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu  
85 90 95

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys  
100 105 110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe  
115 120 125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly  
130 135 140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr  
145 150 155 160

Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe  
165 170 175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys  
180 185 190

Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg  
195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr  
210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg  
225 230 235 240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val  
245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro  
260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser  
275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys  
290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Asp His Asp Gly Leu Met Thr  
305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu  
325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro  
340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr  
355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met  
370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile  
385 390 395 400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg  
405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn  
420 425 430

Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro  
435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His  
450 455 460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro  
465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro  
485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu  
500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val  
515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp  
530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly  
545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser  
565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg  
580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg  
595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr  
610 615 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn  
625 630 635 640

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu  
645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr  
660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln  
675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly

690

695

700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu  
705 710 715 720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr  
725 730 735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu  
740 745 750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val  
755 760 765

Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val  
770 775 780

Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr  
785 790 795 800

Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys  
805 810 815

Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr  
820 825 830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp  
835 840 845

Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys  
850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys  
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro  
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg  
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala  
915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu  
930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu  
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly  
965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn  
980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr  
995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His  
1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr  
1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly  
1040 1045 1050

Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr  
1055 1060 1065

Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp  
1070 1075 1080

Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly  
1085 1090 1095

Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu  
1100 1105 1110

Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser  
1115 1120 1125

Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe  
1130 1135 1140

Asp Gln Ala Gly Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu  
1145 1150 1155

Arg Ser Asp Ala Asp Thr Ala  
1160 1165

<210> 3  
<211> 5099  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (702)..(4196)  
<223>

<220>  
<221> mutation  
<222> (1987)..(1987)  
<223> Substitution of adenine by thymine

<220>  
<221> mutation  
<222> (1288)..(1288)  
<223> Substitution of cytosine by thymine

<220>  
<221> mutation  
<222> (715)..(715)  
<223> Substitution of cytosine by thymine

<400> 3  
acaatgtgac tcgtgatttt tgggtggatc agcgtaccgg tttgggttgc gatctagctg 60  
aaaatattga tgattttac ggcgaccgca gcggccagaa gtacgaacag aaattgcttt 120  
tcgacgcctc cctcgacgat gcagctgtct ctaagctggc tgcacaggcc gaaagcatcc 180  
ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggt gcggtattgg 240  
ctctcggtgg cctggccggg tgaaaaatggaa gaaacgtcga gaagcttaac 300  
ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tggttgcgt 360  
ggtgccctcgta agaagggttc aagaagattt ctggaaaacg cgcccggtcg gttgggtgct 420  
aatagcacgc ggagcaccag atgaaaaatc tccccttac ttccgcgcgc gattggata 480  
ctctgagtcg ttgcgttggaa attcgtgact cttttcggtt cctgtagcgc caagaccttg 540

atcaagggtgg tttaaaaaaaaa ccgatttac aaggcatcc agtgctatct ggagtcgttc	600
agggggatcg ggccctcag cagaccaatt gctaaaaat accagcgtg ttgatctgca	660
cttaatggcc ttgaccagcc aggtgcaatt acccgctga g gtg ctg gaa gga ctc Val Leu Glu Gly Leu	716
1 5	
atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly	764
10 15 20	
gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val	812
25 30 35	
ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly	860
40 45 50	
acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala	908
55 60 65	
cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Leu Ser Pro Ile	956
70 75 80 85	
cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe	1004
90 95 100	
gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn	1052
105 110 115	
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr	1100
120 125 130	
ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met	1148
135 140 145	
acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val	1196
150 155 160 165	
agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp	1244
170 175 180	
aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct ttc cgt Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Phe Arg	1292
185 190 195	
ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt	1340

Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val			
200	205	210	
cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct			1388
Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala			
215	220	225	
ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa			1436
Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu			
230	235	240	245
atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag			1484
Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu			
250	255	260	
gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc			1532
Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr			
265	270	275	
cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag			1580
Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys			
280	285	290	
cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc			1628
Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu			
295	300	305	
ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac			1676
Gly Leu Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp			
310	315	320	325
atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc			1724
Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg			
330	335	340	
gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac			1772
Val Met Thr Ser Pro Asn Gly Glu Ile Pro Val Glu Thr Asp Asp			
345	350	355	
atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc			1820
Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile			
360	365	370	
cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt			1868
Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg			
375	380	385	
gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg			1916
Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu			
390	395	400	405
atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act			1964
Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr			
410	415	420	
tcc cag ctg tct cag ttc atg gtc cag aac aac tcc ctg tct ggt ttg			2012
Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn Ser Leu Ser Gly Leu			

425

430

435

act cac aag cgt cgt ctg tcg gct ctg ggc ccg ggt ggt ctg tcc cgt	2060																																																																																																										
Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg																																																																																																											
440	445	450		gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc	2108	Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly		455	460	465		cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156	Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile		470	475	480	485	ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204	Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu		490	495	500		acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252	Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp		505	510	515		tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc gca aac	2300	Tyr Leu Thr Ala Asp Glu Asp Arg Phe Val Val Ala Gln Ala Asn		520	525	530		acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val		535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660	
450																																																																																																											
gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc	2108																																																																																																										
Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly																																																																																																											
455	460	465		cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156	Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile		470	475	480	485	ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204	Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu		490	495	500		acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252	Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp		505	510	515		tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc gca aac	2300	Tyr Leu Thr Ala Asp Glu Asp Arg Phe Val Val Ala Gln Ala Asn		520	525	530		acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val		535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660									
465																																																																																																											
cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc	2156																																																																																																										
Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile																																																																																																											
470	475	480	485	ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204	Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu		490	495	500		acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252	Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp		505	510	515		tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc gca aac	2300	Tyr Leu Thr Ala Asp Glu Asp Arg Phe Val Val Ala Gln Ala Asn		520	525	530		acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val		535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																	
480	485																																																																																																										
ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag	2204																																																																																																										
Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu																																																																																																											
490	495	500		acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252	Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp		505	510	515		tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc gca aac	2300	Tyr Leu Thr Ala Asp Glu Asp Arg Phe Val Val Ala Gln Ala Asn		520	525	530		acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val		535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																									
500																																																																																																											
acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac	2252																																																																																																										
Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp																																																																																																											
505	510	515		tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc gca aac	2300	Tyr Leu Thr Ala Asp Glu Asp Arg Phe Val Val Ala Gln Ala Asn		520	525	530		acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val		535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																	
515																																																																																																											
tac ctt acc gct gat gag gaa gac cgc ttc gtt gtc gca aac	2300																																																																																																										
Tyr Leu Thr Ala Asp Glu Asp Arg Phe Val Val Ala Gln Ala Asn																																																																																																											
520	525	530		acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348	Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val		535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																									
530																																																																																																											
acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt	2348																																																																																																										
Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp Glu Thr Val Thr Val																																																																																																											
535	540	545		cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396	Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp		550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																	
545																																																																																																											
cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat	2396																																																																																																										
Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp																																																																																																											
550	555	560	565	tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444	Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met		570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																									
560	565																																																																																																										
tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg	2444																																																																																																										
Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met																																																																																																											
570	575	580		att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492	Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala		585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																																	
580																																																																																																											
att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg	2492																																																																																																										
Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala																																																																																																											
585	590	595		aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540	Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe		600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																																									
595																																																																																																											
aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc	2540																																																																																																										
Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe																																																																																																											
600	605	610		gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588	Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu		615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																																																	
610																																																																																																											
gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg	2588																																																																																																										
Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu																																																																																																											
615	620	625		gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636	Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe		630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																																																									
625																																																																																																											
gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc	2636																																																																																																										
Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe																																																																																																											
630	635	640	645	atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684	Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg		650	655	660																																																																																																	
640	645																																																																																																										
atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt	2684																																																																																																										
Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg																																																																																																											
650	655	660																																																																																																									
660																																																																																																											

aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu 665 670 675	2732
gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly 680 685 690	2780
cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val 695 700 705	2828
gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu 710 715 720 725	2876
aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu 730 735 740	2924
gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile 745 750 755	2972
acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp 760 765 770	3020
gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile 775 780 785	3068
ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu 790 795 800 805	3116
gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg 810 815 820	3164
gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly 825 830 835	3212
gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp Leu Ala Pro Gly Val 840 845 850	3260
aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp 855 860 865	3308
ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys 870 875 880 885	3356

att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val 890 895 900	3404
gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly 905 910 915	3452
cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser 920 925 930	3500
gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro 935 940 945	3548
gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val 950 955 960 965	3596
ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser 970 975 980	3644
cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala 985 990 995	3692
acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val 1000 1005 1010	3737
tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp 1015 1020 1025	3782
gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr 1030 1035 1040	3827
cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe 1045 1050 1055	3872
ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr 1060 1065 1070	3917
aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly 1075 1080 1085	3962
cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro 1090 1095 1100	4007
gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc	4052

Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu	
1105 1110 1115	
cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act	4097
Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr	
1120 1125 1130	
cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc	4142
Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly	
1135 1140 1145	
gcc tca ctt ggc atc aac ctg tcc cgt gac gag cgt tcc gac gcc	4187
Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu Arg Ser Asp Ala	
1150 1155 1160	
gac acc gca tagcagatca gaaaacaacc gctagaaaatc aagccataca	4236
Asp Thr Ala	
1165	
tccccggac attgaagaga tgttctgggg ggaaaggag ttttacgtgc tcgacgtaaa	4296
cgtttcgat gagctccgca tcggcctggc caccggcgac gacatccgcc gttggtccaa	4356
gggtgaggtc aagaagccgg agaccatcaa ctaccgaacc ctcaagcctg agaaggacgg	4416
tctgttctgc gagcgtatct tcggtccaac tcgcgactgg gagtgcgcct gcggtaagta	4476
caagcgtgtc cgctacaagg gcatcatctg tgaacgctgt ggcgttgagg tcaccaagtc	4536
caaggtgcgc cgtgagcgc a tgggacacat tgagctcgct gcaccagtaa cccacatttgc	4596
gtacttcaag ggcgttccat cacggctcgg ctacctttt gaccttgctc caaaggacct	4656
ggacctcatc atctacttcg gtgcgaacat catcaccagc gtggacgaag aggctcgcca	4716
cagcgaccag accactctt aggcagaaat gcttctggag aagaaggacg ttgaggcaga	4776
cgcagagtct gacattgctg agcgtgctga aaagctcgaa gaggatctt gctgaacttga	4836
ggcagctggc gctaaggccg acgctcgccg caaggttcag gctgctgccg ataaggaaat	4896
gcagcacatc cgtgagcgtg cacagcgcga aatcgatcgt ctcgatgagg tctggcagac	4956
cttcatcaag cttgctccaa agcagatgat ccgcgatgag aagctctacg atgaactgat	5016
cgaccgctac gaggattact tcaccggtgg tatgggtgca gagtccattt gaggcttgc	5076
ccagaacttc gaccttgatg ctg	5099

<210> 4  
 <211> 1165  
 <212> PRT  
 <213> *Corynebacterium glutamicum*

<400> 4

Val Leu Glu Gly Leu Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val  
1 5 10 15

Val Asp Ile Pro Gly Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser  
20 25 30

Ala Pro Ile Glu Val Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr  
35 40 45

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu  
50 55 60

Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu  
65 70 75 80

Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu  
85 90 95

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys  
100 105 110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe  
115 120 125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly  
130 135 140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr  
145 150 155 160

Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe  
165 170 175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys  
180 185 190

Val Ile Pro Phe Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg  
195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr  
210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg

225 230 235 240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val  
245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro  
260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser  
275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys  
290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr  
305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu  
325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro  
340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr  
355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met  
370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile  
385 390 395 400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg  
405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Val Gln Asn Asn  
420 425 430

Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro  
435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His  
450 455 460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro  
465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro  
485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu  
500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val  
515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp  
530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly  
545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser  
565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg  
580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg  
595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr  
610 615 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn  
625 630 635 640

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu  
645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr  
660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln  
675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly  
690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu  
705 710 715 720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr  
725 730 735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu  
740 745 750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val  
755 760 765

Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val  
770 775 780

Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr  
785 790 795 800

Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys  
805 810 815

Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr  
820 825 830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp  
835 840 845

Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys  
850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys  
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro  
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg  
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala  
915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu  
930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu  
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly  
965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn  
980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr  
995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His  
1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr  
1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly  
1040 1045 1050

Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr  
1055 1060 1065

Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp  
1070 1075 1080

Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly  
1085 1090 1095

Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu  
1100 1105 1110

Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser  
1115 1120 1125

Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe

1130

1135

1140

Asp Gln Ala Gly Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu  
1145 1150 1155

Arg Ser Asp Ala Asp Thr Ala  
1160 1165

<210> 5  
<211> 5099  
<212> DNA  
<213> *Corynebacterium glutamicum*

<220>  
<221> CDS  
<222> (702)..(4196)  
<223>

<220>  
<221> mutation  
<222> (2016)..(2016)  
<223> Substitution of cytosine by thymine

<400> 5  
acaatgtgac tcgtgatttt tgggtggatc agcgtaccgg tttgggtgtc gatctagctg 60  
aaaatattga tgatTTTAC ggcgaccgca gcggccagaa gtacgaacag aaattgcttt 120  
tcgacgcctc cctcgacgat gcagctgtct ctaagctggc tgcacaggcc gaaagcatcc 180  
ctgatggaga tgtgagcaaa atcgcaaata ccgtaggtat tgtgatcggt gcggtattgg 240  
ctctcggtgg cctggccggg tgggggggg cggtggaa gaaacgtcga gaagcttaac 300  
ctgctgttca aatagatttt ccctgtttcg aattgcggaa accccgggtt tgTTTGTAG 360  
gggcctcgta agaaggggtc aagaagattt ctggaaacg cggccgtcgc gttgggtgct 420  
aatagcacgc ggagcaccag atgaaaaatc tccccttac ttgcgcgc gattggata 480  
ctctgagtcg ttgcgttggaa attcgtgact cttttcggtt cctgtagcgc caagaccttg 540  
atcaagggtgg tttaaaaaaa ccgatttgac aaggtcattc agtgctatct ggagtcgttc 600  
agggggatcg ggttcctcag cagaccaatt gctaaaaat accagcggtg ttgatctgca 660  
cttaatggcc ttgaccagcc aggtgcaatt acccgctga g gtg ctg gaa gga ccc 716  
Val Leu Glu Gly Pro  
1 5  
atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 764  
Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly

10	15	20	
gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val 25	30	35	812
ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly 40	45	50	860
acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala 55	60	65	908
cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Leu Ser Pro Ile 70	75	80	956
cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe 90	95	100	1004
gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn 105	110	115	1052
tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr 120	125	130	1100
ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met 135	140	145	1148
acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val 150	155	160	1196
agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp 170	175	180	1244
aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg 185	190	195	1292
ggt gct tgg ctt gag ttt gac gtc gat aag cgc gat tcg gtt ggt gtt Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg Asp Ser Val Gly Val 200	205	210	1340
cgt att gac cgc aag cgt cgc cag cca gtc acc gta ctg ctg aag gct Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr Val Leu Leu Lys Ala 215	220	225	1388
ctt ggc tgg acc act gag cag atc acc gag cgt ttc ggt ttc tct gaa Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg Phe Gly Phe Ser Glu 230	235	240	1436
			245

atc atg atg tcc acc ctc gag tcc gat ggt gta gca aac acc gat gag Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val Ala Asn Thr Asp Glu 250 255 260	1484
gca ttg ctg gag atc tac cgc aag cag cgt cca ggc gag cag cct acc Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro Gly Glu Gln Pro Thr 265 270 275	1532
cgc gac ctt gcg cag tcc ctc ctg gac aac agc ttc ttc cgt gca aag Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser Phe Phe Arg Ala Lys 280 285 290	1580
cgc tac gac ctg gct cgc gtt ggt cgt tac aag atc aac cgc aag ctc Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys Ile Asn Arg Lys Leu 295 300 305	1628
ggc ctt ggt ggc gac cac gat ggt ttg atg act ctt act gaa gag gac Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr Leu Thr Glu Glu Asp 310 315 320 325	1676
atc gca acc acc atc gag tac ctg gtg cgt ctg cac gca ggt gag cgc Ile Ala Thr Ile Glu Tyr Leu Val Arg Leu His Ala Gly Glu Arg 330 335 340	1724
gtc atg act tct cca aat ggt gaa gag atc cca gtc gag acc gat gac Val Met Thr Ser Pro Asn Gly Glu Ile Pro Val Glu Thr Asp Asp 345 350 355	1772
atc gac cac ttt ggt aac cgt cgt ctg cgt acc gtt ggc gaa ctg atc Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr Val Gly Glu Leu Ile 360 365 370	1820
cag aac cag gtc cgt gtc ggc ctg tcc cgc atg gag cgc gtt gtt cgt Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met Glu Arg Val Val Arg 375 380 385	1868
gag cgt atg acc acc cag gat gcg gag tcc att act cct act tcc ttg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile Thr Pro Thr Ser Leu 390 395 400 405	1916
atc aac gtt cgt cct gtc tct gca gct atc cgt gag ttc ttc gga act Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg Glu Phe Phe Gly Thr 410 415 420	1964
tcc cag ctg tct cag ttc atg gac cag aac aac tcc ctg tct ggt ttg Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn Ser Leu Ser Gly Leu 425 430 435	2012
act tac aag cgt cgt tcg gct ctg ggc ccg ggt ggt ctg tcc cgt Thr Tyr Lys Arg Arg Leu Ser Ala Leu Gly Pro Gly Gly Leu Ser Arg 440 445 450	2060
gag cgc gcc ggc atc gag gtt cga gac gtt cac cca tct cac tac ggc Glu Arg Ala Gly Ile Glu Val Arg Asp Val His Pro Ser His Tyr Gly 455 460 465	2108

cgt atg tgc cca att gag act ccg gaa ggt cca aac att ggc ctg atc Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro Asn Ile Gly Leu Ile 470 475 480 485	2156
ggt tcc ttg gct tcc tat gct cga gtg aac cca ttc ggt ttc att gag Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro Phe Gly Phe Ile Glu 490 495 500	2204
acc cca tac cgt cgc atc atc gac ggc aag ctg acc gac cag att gac Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu Thr Asp Gln Ile Asp 505 510 515	2252
tac ctt acc gct gat gag gaa gac cgc ttc gtt gtt gcg cag gca aac Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val Val Ala Gln Ala Asn 520 525 530	2300
acg cac tac gac gaa gag ggc aac atc acc gat gag acc gtc act gtt Thr His Tyr Asp Glu Glu Asn Ile Thr Asp Glu Thr Val Thr Val 535 540 545	2348
cgt ctg aag gac ggc gac atc gcc atg gtt ggc cgc aac gcg gtt gat Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly Arg Asn Ala Val Asp 550 555 560 565	2396
tac atg gac gtt tcc cct cgt cag atg gtt tct gtt ggt acc gcg atg Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser Val Gly Thr Ala Met 570 575 580	2444
att cca ttc ctg gag cac gac gat gct aac cgt gca ctg atg ggc gcg Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg Ala Leu Met Gly Ala 585 590 595	2492
aac atg cag aag cag gct gtg cca ctg att cgt gcc gag gct cct ttc Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg Ala Glu Ala Pro Phe 600 605 610	2540
gtg ggc acc ggt atg gag cag cgc gca gca tac gac gcc ggc gac ctg Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr Asp Ala Gly Asp Leu 615 620 625	2588
gtt att acc cca gtc gca ggt gtg gtg gaa aac gtt tca gct gac ttc Val Ile Thr Pro Val Ala Gly Val Val Glu Asn Val Ser Ala Asp Phe 630 635 640 645	2636
atc acc atc atg gct gat gac ggc aag cgc gaa acc tac ctg ctg cgt Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu Thr Tyr Leu Leu Arg 650 655 660	2684
aag ttc cag cgc acc aac cag ggc acc agc tac aac cag aag cct ttg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr Asn Gln Lys Pro Leu 665 670 675	2732
gtt aac ttg ggc gag cgc gtt gaa gct ggc cag gtt att gct gat ggt Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln Val Ile Ala Asp Gly 680 685 690	2780
cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt	2828

Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val			
695	700	705	
gct ttc atg cct tgg gaa ggc cac aac tac gag gat gct atc atc ctc			2876
Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu			
710	715	720	725
aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag			2924
Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu			
730	735	740	
gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc			2972
Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile			
745	750	755	
acc cgc gac atc cct aat gtg tct gaa gaa gtc ctc aag gac ctc gac			3020
Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp			
760	765	770	
gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc			3068
Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile			
775	780	785	
ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccc gaa			3116
Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu			
790	795	800	805
gag cgc ttg ctg cgc gca atc ttc ggt gag aag gcc cgc gaa gtt cgc			3164
Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg			
810	815	820	
gat acc tcc atg aag gtg cct cac ggt gag acc ggc aag gtc atc ggc			3212
Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly			
825	830	835	
gtg cgt cac ttc tcc cgc gag gac gac gat ctg gct cct ggc gtc			3260
Val Arg His Phe Ser Arg Glu Asp Asp Asp Leu Ala Pro Gly Val			
840	845	850	
aac gag atg atc cgt atc tac gtt gct cag aag cgt aag atc cag gac			3308
Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys Arg Lys Ile Gln Asp			
855	860	865	
ggc gat aag ctc gct ggc cgc cac ggt aac aag ggt gtt gtc ggt aaa			3356
Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys Gly Val Val Gly Lys			
870	875	880	885
att ttg cct cag gaa gat atg cca ttc ctt cca gac ggc act cct gtt			3404
Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro Asp Gly Thr Pro Val			
890	895	900	
gac atc atc ttg aac acc cac ggt gtt cca cgt cgt atg aac att ggt			3452
Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg Arg Met Asn Ile Gly			
905	910	915	
cag gtt ctt gag acc cac ctt ggc tgg ctg gca tct gct ggt tgg tcc			3500
Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala Ser Ala Gly Trp Ser			

920	925	930	
gtg gat cct gaa gat cct gag aac gct gag ctc gtc aag act ctg cct Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu Val Lys Thr Leu Pro 935	940	945	3548
gca gac ctc ctc gag gtt cct gct ggt tcc ttg act gca act cct gtg Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu Thr Ala Thr Pro Val 950	955	960	3596
ttc gac ggt gcg tca aac gaa gag ctc gca ggc ctg ctc gct aat tca Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly Leu Leu Ala Asn Ser 970	975	980	3644
cgt cca aac cgc gac ggc gac gtc atg gtt aac gcg gat ggt aaa gca Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn Ala Asp Gly Lys Ala 985	990	995	3692
acg ctt atc gac ggt cgc tcc ggt gag cct tac ccg tac ccg gtt Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr Pro Tyr Pro Val 1000	1005	1010	3737
tcc atc ggc tac atg tac atg ctg aag ctg cac cac ctc gtt gac Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His His Leu Val Asp 1015	1020	1025	3782
gag aag atc cac gca cgt tcc act ggt cct tac tcc atg att acc Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr Ser Met Ile Thr 1030	1035	1040	3827
cag cag cca ctg ggt ggt aaa gca cag ttc ggt gga cag cgt ttc Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly Gly Gln Arg Phe 1045	1050	1055	3872
ggc gaa atg gag gtg tgg gca atg cag gca tac ggc gct gcc tac Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr Gly Ala Ala Tyr 1060	1065	1070	3917
aca ctt cag gag ctg ctg acc atc aag tct gat gac gtg gtt ggc Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp Asp Val Val Gly 1075	1080	1085	3962
cgt gtc aag gtc tac gaa gca att gtg aag ggc gag aac atc ccg Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly Glu Asn Ile Pro 1090	1095	1100	4007
gat cca ggt att cct gag tcc ttc aag gtt ctc ctc aag gag ctc Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu Leu Lys Glu Leu 1105	1110	1115	4052
cag tcc ttg tgc ctg aac gtg gag gtt ctc tcc gca gac ggc act Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser Ala Asp Gly Thr 1120	1125	1130	4097
cca atg gag ctc gcg ggt gac gac gac gac ttc gat cag gca ggc Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe Asp Gln Ala Gly 1135	1140	1145	4142

gcc tca ctt	ggc atc aac ctg tcc	cgt gac gag cgt tcc	gac gcc	4187
Ala Ser Leu	Gly Ile Asn Leu Ser	Arg Asp Glu Arg Ser	Asp Ala	
1150	1155	1160		
gac acc gca	tagcagatca gaaaacaacc	gctagaaaatc	aagccataca	4236
Asp Thr Ala				
1165				
tcccccggac	attgaagaga	tgttctgggg	ggaaaggag	4296
cgtcttcgat	gagctccgca	tcggcctggc	caccgcccac	4356
gggtgaggtc	aagaagccgg	agaccatcaa	ctaccgaacc	4416
tctgttctgc	gagcgtatct	tcggtccaa	tcgactgg	4476
caagcgtgtc	cgctacaagg	gcatcatctg	tgaacgctgt	4536
caaggtgcgc	cgtgagcgca	tgggacacat	ttagctcgct	4596
gtacttcaag	ggcggtccat	cacgcctcg	ctacctttg	4656
ggacctcatc	atctacttcg	gtgcgaacat	catcaccagc	4716
cagcgaccag	accactttg	aggcagaaat	gcttctggag	4776
cgcagagtct	gacattgctg	agcgtgctga	aaagctcgaa	4836
ggcagctggc	gctaaggccg	acgctcgccg	caaggttcag	4896
gcagcacatc	cgtgagcggt	cacagcgca	aatcgatcgt	4956
cttcatcaag	cttgctccaa	agcagatgat	ccgcgatgag	5016
cgaccgctac	gaggattact	tcaccgggtgg	tatgggtgca	5076
ccagaacttc	gaccttcatg	ctg		5099

<210> 6  
 <211> 1165  
 <212> PRT  
 <213> *Corynebacterium glutamicum*  
 <400> 6

Val	Leu	Glu	Gly	Pro	Ile	Leu	Ala	Val	Arg	Gln	Thr	Lys	Ser	Val
1				5				10				15		

Val	Asp	Ile	Pro	Gly	Ala	Pro	Gln	Arg	Tyr	Ser	Phe	Ala	Lys	Val	Ser
								20	25			30			

Ala	Pro	Ile	Glu	Val	Pro	Gly	Leu	Leu	Asp	Leu	Gln	Leu	Asp	Ser	Tyr
									35	40		45			

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu  
50 55 60

Phe Gly Glu Gly Ala Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu  
65 70 75 80

Glu Leu Ser Pro Ile Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu  
85 90 95

Ser Glu Pro Arg Phe Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys  
100 105 110

Glu Lys Asp Ile Asn Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe  
115 120 125

Val Asn Asn Thr Thr Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly  
130 135 140

Asp Phe Pro Met Met Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr  
145 150 155 160

Glu Arg Val Val Val Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe  
165 170 175

Asp Gln Thr Ile Asp Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys  
180 185 190

Val Ile Pro Ser Arg Gly Ala Trp Leu Glu Phe Asp Val Asp Lys Arg  
195 200 205

Asp Ser Val Gly Val Arg Ile Asp Arg Lys Arg Arg Gln Pro Val Thr  
210 215 220

Val Leu Leu Lys Ala Leu Gly Trp Thr Thr Glu Gln Ile Thr Glu Arg  
225 230 235 240

Phe Gly Phe Ser Glu Ile Met Met Ser Thr Leu Glu Ser Asp Gly Val  
245 250 255

Ala Asn Thr Asp Glu Ala Leu Leu Glu Ile Tyr Arg Lys Gln Arg Pro  
260 265 270

Gly Glu Gln Pro Thr Arg Asp Leu Ala Gln Ser Leu Leu Asp Asn Ser  
275 280 285

Phe Phe Arg Ala Lys Arg Tyr Asp Leu Ala Arg Val Gly Arg Tyr Lys  
290 295 300

Ile Asn Arg Lys Leu Gly Leu Gly Gly Asp His Asp Gly Leu Met Thr  
305 310 315 320

Leu Thr Glu Glu Asp Ile Ala Thr Thr Ile Glu Tyr Leu Val Arg Leu  
325 330 335

His Ala Gly Glu Arg Val Met Thr Ser Pro Asn Gly Glu Glu Ile Pro  
340 345 350

Val Glu Thr Asp Asp Ile Asp His Phe Gly Asn Arg Arg Leu Arg Thr  
355 360 365

Val Gly Glu Leu Ile Gln Asn Gln Val Arg Val Gly Leu Ser Arg Met  
370 375 380

Glu Arg Val Val Arg Glu Arg Met Thr Thr Gln Asp Ala Glu Ser Ile  
385 390 395 400

Thr Pro Thr Ser Leu Ile Asn Val Arg Pro Val Ser Ala Ala Ile Arg  
405 410 415

Glu Phe Phe Gly Thr Ser Gln Leu Ser Gln Phe Met Asp Gln Asn Asn  
420 425 430

Ser Leu Ser Gly Leu Thr Tyr Lys Arg Arg Leu Ser Ala Leu Gly Pro  
435 440 445

Gly Gly Leu Ser Arg Glu Arg Ala Gly Ile Glu Val Arg Asp Val His  
450 455 460

Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro  
465 470 475 480

Asn Ile Gly Leu Ile Gly Ser Leu Ala Ser Tyr Ala Arg Val Asn Pro  
485 490 495

Phe Gly Phe Ile Glu Thr Pro Tyr Arg Arg Ile Ile Asp Gly Lys Leu  
500 505 510

Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val  
515 520 525

Val Ala Gln Ala Asn Thr His Tyr Asp Glu Glu Gly Asn Ile Thr Asp  
530 535 540

Glu Thr Val Thr Val Arg Leu Lys Asp Gly Asp Ile Ala Met Val Gly  
545 550 555 560

Arg Asn Ala Val Asp Tyr Met Asp Val Ser Pro Arg Gln Met Val Ser  
565 570 575

Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg  
580 585 590

Ala Leu Met Gly Ala Asn Met Gln Lys Gln Ala Val Pro Leu Ile Arg  
595 600 605

Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr  
610 615 620

Asp Ala Gly Asp Leu Val Ile Thr Pro Val Ala Gly Val Val Glu Asn  
625 630 635 640

Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu  
645 650 655

Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr  
660 665 670

Asn Gln Lys Pro Leu Val Asn Leu Gly Glu Arg Val Glu Ala Gly Gln  
675 680 685

Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly  
690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu  
705 710 715 720

Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr

725

730

735

Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu  
740 745 750

Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val  
755 760 765

Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val  
770 775 780

Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr  
785 790 795 800

Glu Leu Thr Pro Glu Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys  
805 810 815

Ala Arg Glu Val Arg Asp Thr Ser Met Lys Val Pro His Gly Glu Thr  
820 825 830

Gly Lys Val Ile Gly Val Arg His Phe Ser Arg Glu Asp Asp Asp Asp  
835 840 845

Leu Ala Pro Gly Val Asn Glu Met Ile Arg Ile Tyr Val Ala Gln Lys  
850 855 860

Arg Lys Ile Gln Asp Gly Asp Lys Leu Ala Gly Arg His Gly Asn Lys  
865 870 875 880

Gly Val Val Gly Lys Ile Leu Pro Gln Glu Asp Met Pro Phe Leu Pro  
885 890 895

Asp Gly Thr Pro Val Asp Ile Ile Leu Asn Thr His Gly Val Pro Arg  
900 905 910

Arg Met Asn Ile Gly Gln Val Leu Glu Thr His Leu Gly Trp Leu Ala  
915 920 925

Ser Ala Gly Trp Ser Val Asp Pro Glu Asp Pro Glu Asn Ala Glu Leu  
930 935 940

Val Lys Thr Leu Pro Ala Asp Leu Leu Glu Val Pro Ala Gly Ser Leu  
945 950 955 960

Thr Ala Thr Pro Val Phe Asp Gly Ala Ser Asn Glu Glu Leu Ala Gly  
965 970 975

Leu Leu Ala Asn Ser Arg Pro Asn Arg Asp Gly Asp Val Met Val Asn  
980 985 990

Ala Asp Gly Lys Ala Thr Leu Ile Asp Gly Arg Ser Gly Glu Pro Tyr  
995 1000 1005

Pro Tyr Pro Val Ser Ile Gly Tyr Met Tyr Met Leu Lys Leu His  
1010 1015 1020

His Leu Val Asp Glu Lys Ile His Ala Arg Ser Thr Gly Pro Tyr  
1025 1030 1035

Ser Met Ile Thr Gln Gln Pro Leu Gly Gly Lys Ala Gln Phe Gly  
1040 1045 1050

Gly Gln Arg Phe Gly Glu Met Glu Val Trp Ala Met Gln Ala Tyr  
1055 1060 1065

Gly Ala Ala Tyr Thr Leu Gln Glu Leu Leu Thr Ile Lys Ser Asp  
1070 1075 1080

Asp Val Val Gly Arg Val Lys Val Tyr Glu Ala Ile Val Lys Gly  
1085 1090 1095

Glu Asn Ile Pro Asp Pro Gly Ile Pro Glu Ser Phe Lys Val Leu  
1100 1105 1110

Leu Lys Glu Leu Gln Ser Leu Cys Leu Asn Val Glu Val Leu Ser  
1115 1120 1125

Ala Asp Gly Thr Pro Met Glu Leu Ala Gly Asp Asp Asp Asp Phe  
1130 1135 1140

Asp Gln Ala Gly Ala Ser Leu Gly Ile Asn Leu Ser Arg Asp Glu  
1145 1150 1155

Arg Ser Asp Ala Asp Thr Ala  
1160 1165

<210> 7  
<211> 1775  
<212> DNA  
<213> **Corynebacterium glutamicum**

<220>  
<221> CDS  
<222> (500)..(880)  
<223>

<400> 7  
cagctctaca agagtgtcta agtggcgggc attccatgct ttggaggagc gatttcaaa 60  
ttcctccaaa gtgagttgac ctcggaaac agctgcagaa agttcatcca cgacttggtt 120  
tcggttaagg tcagtggcga gcttcttgc tggttcgaaa ctttgaggaa cagtcatggg 180  
aaccattcta acaagggatt tggtgtttc tgccgcttagc tgataatgtg aacggctgag 240  
tcccactctt gtagttggga attgacggca cctcgactc aagcgcggta tcgccccctgg 300  
tttccggga cgcggggcg catgttgca tttgatgagg ttgtccgtga catgtttgg 360  
cggcccccaa aaagagcccc ctttttgcg tgtctggaca cttttcaaa tccttcgcca 420  
tcgacaagct cagccttcgt gttcgcccc cggcgctcac gtcagcagtt aaagaacaac 480  
tccgaaataa ggatggttc atg cca act att cag cag ctg gtc cgt aag ggc 532  
Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly  
1 5 10  
cgc cac gat aag tcc gcc aag gtg gct acc gcg gca ctg aag ggt tcc 580  
Arg His Asp Lys Ser Ala Lys Val Ala Thr Ala Leu Lys Gly Ser  
15 20 25  
cct cag cgt cgt ggc gta tgc acc cgt gtg tac acc acc acc cct aag 628  
Pro Gln Arg Arg Gly Val Cys Thr Arg Val Tyr Thr Thr Pro Lys  
30 35 40  
aag cct aac tct gct ctt cgt aag gtc gct cgt gtg cgc ctt acc tcc 676  
Lys Pro Asn Ser Ala Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser  
45 50 55  
ggc atc gag gtt tcc gct tac atc cct ggt gag ggc cac aac ctg cag 724  
Gly Ile Glu Val Ser Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln  
60 65 70 75  
gag cac tcc atg gtg ctc gtt cgc ggt cgt gtt aag gac ctc cca 772  
Glu His Ser Met Val Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro  
80 85 90  
ggt gtc cgt tac aag atc gtc cgt ggc gca ctg gat acc cag ggt gtt 820  
Gly Val Arg Tyr Lys Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val  
95 100 105

aag gac cgc aag cag gct cgt tcc ccg cta cg	gaa gag ggg ata	868													
Lys Asp Arg Lys Gln Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile															
110	115	120													
att aaa aat gcg taaatcagca gctcctaagc gtccagtagt tcaggaccct		920													
Ile Lys Asn Ala															
125															
gtatacaga	ccgagctcg	tacccagctc	gtaaacaaga	tcctcatcg	tggcaagaag	980									
tccaccgcag	agcgcac	ctacgg	gtca	ctcgagatct	gccgtgagaa	gaccggcacc	1040								
gatccagtag	gaacc	ctcg	gaagg	ctc	ggcaacgtgc	gtccagac	1100								
tcccgccgt	ttgg	ttgg	gc	tac	tacc	gtgc	atgttc	cccc	agag	cg	ca	1160			
aacaccctcg	ca	ct	gcgtt	g	ttgg	taacc	tt	caccc	cg	tc	g	ga	1220		
atcgagcg	tc	tg	caa	ac	tt	ctggat	gc	agcca	ac	gc	tg	cc	1280		
cgtcg	ca	cc	ac	ac	ac	at	gc	cc	cg	cc	gt	ga	1340		
tagtactg	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1400		
cacattt	gaa	ta	ag	ct	gg	ca	gc	ct	tc	cc	gt	tt	1460		
aatgcag	tt	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	cc	1520		
aaaaatccat	gt	ca	ct	tg	cc	tc	cg	gt	tc	cc	gt	cc	tt	1580	
aacaagagaa	tt	at	cc	gt	ta	ac	ct	gt	ca	cc	gt	cc	tt	1640	
cccg	ta	ta	ta	ta	ta	ta	ta	ta	ta	ta	ta	ta	1700		
aagt	gt	ct	ta	aa	ac	ac	gt	cc	gc	ca	tc	at	gat	ct	1760
gta	aa	g	ac	ca	cc	ac	cc	cc	cc	cc	cc	cc	cc	1775	

<210> 8  
 <211> 127  
 <212> PRT  
 <213> Corynebacterium glutamicum

<400> 8

Met Pro Thr Ile Gln Gln Leu Val Arg Lys Gly Arg His Asp Lys Ser			
1	5	10	15

Ala Lys Val Ala Thr Ala Ala Leu Lys Gly Ser Pro Gln Arg Arg Gly			
20	25	30	

Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala			
35	40	45	

Leu Arg Lys Val Ala Arg Val Arg Leu Thr Ser Gly Ile Glu Val Ser  
50 55 60

Ala Tyr Ile Pro Gly Glu Gly His Asn Leu Gln Glu His Ser Met Val  
65 70 75 80

Leu Val Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr Lys  
85 90 95

Ile Val Arg Gly Ala Leu Asp Thr Gln Gly Val Lys Asp Arg Lys Gln  
100 105 110

Ala Arg Ser Pro Leu Arg Arg Glu Glu Gly Ile Ile Lys Asn Ala  
115 120 125

<210> 9  
<211> 24  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 9  
acaatgtgac tcgtgatttt tggg 24

<210> 10  
<211> 20  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 10  
ggaaacgtcc atgtaatcaa 20

<210> 11  
<211> 20  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 11  
aacacgcact acgacgaaaga 20

<210> 12  
<211> 20  
<212> DNA  
<213> ARTIFICIAL SEQUENCE

<220>  
<223> SYNTHETIC DNA

<400> 12  
cagcatcaag gtcgaagttc

20